

**IN THE CLAIMS:**

The claims are pending in the application as follows:

1. (Canceled)
2. (Withdrawn) An oligonucleotide array comprising multiple subblock regions and oligonucleotides with different base sequences positioned to each of said multiple subblock regions, wherein said oligonucleotides are positioned according to an arrangement pattern wherein oligonucleotides with a first correlation degree are positioned closer to each other than oligonucleotides that have a lower correlation degree.
3. (Withdrawn) The oligonucleotide array according to claim 2 wherein said oligonucleotides are oligonucleotides related to a particular phenotype.
4. (Withdrawn) The oligonucleotide array according to claim 2 wherein said phenotype is related to stress response.
5. (Withdrawn) The oligonucleotide array according to claim 4 wherein said oligonucleotides are one of the following: internal or external standard genes for calibration, stress tolerance or survival related genes and hormonal genes, cytokine genes, apoptosis inducing genes, glucocorticoid and other anti-inflammation related genes and growth repressor genes, immune response related transcription factors and signaling molecules, cell disorder triggering cytokine inductive transcription factors and signaling molecules, growth inhibition related transcription factors and signaling molecules, stress tolerance related transcription factors and signaling molecules.
6. (Withdrawn) The oligonucleotide array according to claim 2 wherein said correlation degrees are those determined in a database.
7. (Withdrawn) The oligonucleotide array according to claim 6 wherein said correlation degrees are determined by one or a combination of two or more of gene inter-

relationship score, pairwise information of ligand and receptor, protein-protein interaction information, and gene pathway information.

8. (Withdrawn) The oligonucleotide array according to claim 2 wherein said correlation degree is statistically calculated from expression amount of experimental results using samples for comparison, wherein classification algorithm used comprises either one of P value, FDD, SVM and others.
9. (Withdrawn) The oligonucleotide array according to claim 8 wherein said samples comprise samples from patients with a particular disease and samples from healthy subjects.
10. (Withdrawn) A method of evaluating label detection of hybridization wherein labeled cell-derived RNA are hybridized to an oligonucleotide array comprising multiple subblock regions and oligonucleotides with different base sequences positioned to each of said multiple subblock regions, wherein said oligo-nucleotides are positioned according to an arrangement pattern wherein oligonucleotides with a first correlation degree are positioned closer to each other than oligonucleotides that have a lower correlation degree; and said hybridization is label detected.
11. (Previously presented) An oligonucleotide array, comprising an array of multiple oligonucleotides with different base sequences fixed onto known and separate positions on a support substrate, wherein said oligonucleotides are only biological stress related genes or complementary sequences to said genes, and said multiple oligonucleotides are classified according to their gene functions wherein the support substrate has fixation regions divided according to said classification, wherein the classification is (1) internal and external standard genes for proofreading, (2) stress-related genes related to heat shock protein and hormone genes that decreases under stress, (3) cytokine genes, (4) genes that induce cell death, (5) genes related to anti-inflammation and wound healing and genes related to cell growth inhibition, (6) transcription factor and signaling molecules related to immune response, (7) induction of cytokine, which causes cell injury, (8) transcription factor and signaling molecules

related to growth inhibition, and (9) transcription factor and signaling molecules related to stress response.

12. (Canceled)